



1600

Does Not Comply  
Corrected Diskette Needed

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/463,494A

DATE: 03/07/2002  
TIME: 11:06:17

Input Set : A:\PTO.VSK.txt  
Output Set: N:\CRF3\03072002\I463494A.raw

## SEQUENCE LISTING

- 4 (1) GENERAL INFORMATION:  
5 (i) APPLICANT: Reetz, Manfred; Zonta, Albin; Schimossek, Klaus;  
6 Liebeton, Klaus; Jager, Karl-Erich  
7 (ii) TITLE OF INVENTION: A Process for the Preparation and  
8 Identification of Novel Hydrolases Having Improved  
9 Properties  
10 (iii) NUMBER OF SEQUENCES: 21  
C--> 11 (iv) CORRESPONDENCE ADDRESS:  
12 (A) ADDRESSEE: Norris McLaughlin & Marcus  
13 (B) STREET: 220 East 42nd Street, 30th Floor  
14 (C) CITY: New York  
15 (D) STATE: New York  
16 (E) COUNTRY: USA  
17 (F) ZIP: 10017  
18 (v) COMPUTER READABLE FORM:  
19 (A) MEDIUM TYPE: Floppy disk  
20 (B) COMPUTER: IBM PC compatible  
21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
23 (vi) CURRENT APPLICATION DATA:  
C--> 24 (A) APPLICATION NUMBER: US/09/463,494A  
C--> 25 (B) FILING DATE: 25-Jul-2000  
26 (C) CLASSIFICATION:  
27 (vii) PRIOR APPLICATION DATA:  
28 (A) APPLICATION NUMBER: PCT/EP98/04612  
29 (B) FILING DATE: 23-JUL-1998  
30 (A) APPLICATION NUMBER: DE 197 31 990.4  
31 (B) FILING DATE: 25-JUL-1997  
32 (viii) ATTORNEY/AGENT INFORMATION:  
33 (A) NAME: Briscoe, Kurt G.  
34 (B) REGISTRATION NUMBER: 33141  
35 (C) REFERENCE/DOCKET NUMBER: STUDIEN 268  
36 (ix) TELECOMMUNICATION INFORMATION:  
37 (A) TELEPHONE: (212) 808-0700  
38 (B) TELEFAX: (212) 808-0844  
39 (2) INFORMATION FOR SEQ ID NO: 1:  
40 (i) SEQUENCE CHARACTERISTICS:  
41 (A) LENGTH: 30 base pairs  
42 (B) TYPE: nucleic acid  
43 (C) STRANDEDNESS: unknown  
44 (D) TOPOLOGY: linear  
45 (ii) MOLECULE TYPE: other nucleic acid  
46  
47  
48  
49  
50

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```

51      (A) DESCRIPTION: /desc = "synthetic DNA"
53      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
55 GCGCAATTAA CCCTCACTAA AGGGAACAAA
56      (2) INFORMATION FOR SEQ ID NO: 2:
57      (i) SEQUENCE CHARACTERISTICS:
58          (A) LENGTH: 27 base pairs
59          (B) TYPE: nucleic acid
60          (C) STRANDEDNESS: unknown
61          (D) TOPOLOGY: linear
62      (ii) MOLECULE TYPE: other nucleic acid
63      (A) DESCRIPTION: /desc = "synthetic DNA"
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
65 GCGTAATACG ACTCACTATA GGGCGGAA
66      (2) INFORMATION FOR SEQ ID NO: 3:
67      (i) SEQUENCE CHARACTERISTICS:
68          (A) LENGTH: 1049 base pairs
69          (B) TYPE: nucleic acid
70          (C) STRANDEDNESS: unknown
71          (D) TOPOLOGY: unknown
72      (ii) MOLECULE TYPE: DNA (genomic)
73      (ix) FEATURE:
74          (A) NAME/KEY: CDS
75          (B) LOCATION:85..1017
76      (ix) FEATURE:
77          (A) NAME/KEY: mat_peptide
78          (B) LOCATION:163..1017
79      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
80 GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG GCAGGACGCG CCCCTCGGCC
81 CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TAT CTG CTC CCC CTC
82      Met Lys Lys Lys Tyr Leu Leu Pro Leu
83      -26 -25 -20
84 GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG
85 Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ser Pro Leu Ile Gln
86 -15 -10 -5
87 GGC ACC ACC TAC ACC CAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC
88 Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
89 1 5 10 15
90 ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT
91 Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
92 20 25 30
93 CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC
94 Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
95 35 40 45
96 AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG
97 Ser Gln Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
98 50 55 60
99 GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC
100 Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
101 65 70 75

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124 GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT      447
125 Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
126 80                               85                               90                               95
128 CCC GAC CTG ATC GCT TCC GCC ATC AGC GTC GGC GCC CCG CAC AAG GGT      495
129 Pro Asp Leu Ile Ala Ser Ala Ile Ser Val Gly Ala Pro His Lys Gly
130                               100                               105                               110
132 TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC      543
133 Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
134                               115                               120                               125
136 GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC      591
137 Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
138                               130                               135                               140
141 TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG      639
142 Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu
143                               145                               150                               155
145 GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG      687
146 Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
147 160                               165                               170                               175
149 CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC      735
150 Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
151                               180                               185                               190
153 GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC      783
154 Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
155                               195                               200                               205
157 CTC GAT CCG AGC GAC GCC TTC CTC GGC GCC TCG TCG CTG ACC TTC AAG      831
158 Leu Asp Pro Ser Asp Ala Phe Leu Gly Ala Ser Ser Leu Thr Phe Lys
159                               210                               215                               220
161 AAC GGC ACC GCC AAC GAC GGC CTG GTC GGC ACC TGC AGT TCG CAC CTG      879
162 Asn Gly Thr Ala Asn Asp Gly Leu Val Gly Thr Cys Ser Ser His Leu
163                               225                               230                               235
165 GGC ATG GTG ATC CGC GAC AAC TAC CGG ATG AAC CAC CTG GAC GAG GTG      927
166 Gly Met Val Ile Arg Asp Asn Tyr Arg Met Asn His Leu Asp Glu Val
167 240                               245                               250                               255
169 AAC CAG GTC TTC GGC CTC ACC AGC CTG TTC GAG ACC AGC CCG GTC AGC      975
170 Asn Gln Val Phe Gly Leu Thr Ser Leu Phe Glu Thr Ser Pro Val Ser
171                               260                               265                               270
173 GTC TAC CGC CAG CAC GCC AAC CGC CTG AAG AAC GCC AGC CTG      1017
174 Val Tyr Arg Gln His Ala Asn Arg Leu Lys Asn Ala Ser Leu
175                               275                               280                               285
177 TAGGACCCCG GCCGGGGCCT CGGCCCGGGC CC      1049
180 (2) INFORMATION FOR SEQ ID NO: 4:
182 (i) SEQUENCE CHARACTERISTICS:
183 (A) LENGTH: 311 amino acids
184 (B) TYPE: amino acid
185 (D) TOPOLOGY: linear
187 (ii) MOLECULE TYPE: protein
188 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
190 Met Lys Lys Lys Tyr Leu Leu Pro Leu Gly Leu Ala Ile Gly Leu Ala
191 -26 -25 -20 -15

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```

193 Ser Leu Ala Ala Ser Pro Leu Ile Gln Ala Ser Thr Tyr Thr Gln Thr
194 -10 -5 1 5
196 Lys Tyr Pro Ile Val Leu Ala His Gly Met Leu Gly Phe Asp Asn Ile
197 10 15 20
199 Leu Gly Val Asp Tyr Trp Phe Gly Ile Pro Ser Ala Leu Arg Arg Asp
200 25 30 35
203 Gly Ala Gln Val Tyr Val Thr Glu Val Ser Gln Leu Asp Thr Ser Glu
204 40 45 50
206 Val Arg Gly Glu Gln Leu Leu Gln Gln Val Glu Ile Val Ala Leu
207 55 60 65 70
209 Ser Gly Gln Pro Lys Val Asn Leu Ile Gly His Ser His Gly Gly Pro
210 75 80 85
212 Thr Ile Arg Tyr Val Ala Ala Val Arg Pro Asp Leu Ile Ala Ser Ala
213 90 95 100
215 Ile Ser Val Gly Ala Pro His Lys Gly Ser Asp Thr Ala Asp Phe Leu
216 105 110 115
218 Arg Gln Ile Pro Pro Gly Ser Ala Gly Glu Ala Val Leu Ser Gly Leu
219 120 125 130
221 Val Asn Ser Leu Gly Ala Leu Ile Ser Phe Leu Ser Ser Gly Gly Thr
222 135 140 145 150
224 Gly Thr Gln Asn Ser Leu Gly Ser Leu Glu Ser Leu Asn Ser Glu Gly
225 155 160 165
227 Ala Ala Arg Phe Asn Ala Lys Tyr Pro Gln Gly Ile Pro Thr Ser Ala
228 170 175 180
230 Cys Gly Glu Gly Ala Tyr Lys Val Asn Gly Val Ser Tyr Tyr Ser Trp
231 185 190 195
233 Ser Gly Ser Ser Pro Leu Thr Asn Phe Leu Asp Pro Ser Asp Ala Phe
234 200 205 210
236 Leu Gly Ala Ser Ser Leu Thr Phe Lys Asn Gly Thr Ala Asn Asp Gly
237 215 220 225 230
239 Leu Val Gly Thr Cys Ser Ser His Leu Gly Met Val Ile Arg Asp Asn
240 235 240 245
242 Tyr Arg Met Asn His Leu Asp Glu Val Asn Gln Val Phe Gly Leu Thr
243 250 255 260
245 Ser Leu Phe Glu Thr Ser Pro Val Ser Val Tyr Arg Gln His Ala Asn
246 265 270 275
248 Arg Leu Lys Asn Ala Ser Leu
249 280 285
252 (2) INFORMATION FOR SEQ ID NO: 5:
254 (i) SEQUENCE CHARACTERISTICS:
255 (A) LENGTH: 1049 base pairs
256 (B) TYPE: nucleic acid
257 (C) STRANDEDNESS: unknown
258 (D) TOPOLOGY: unknown
260 (ii) MOLECULE TYPE: DNA (genomic)
262 (ix) FEATURE:
263 (A) NAME/KEY: CDS
264 (B) LOCATION: 85..1017
266 (ix) FEATURE:

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Output Set : N:\CRF3\03072002\I463494A.raw

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267      (A) NAME/KEY: mat_peptide
268      (B) LOCATION:163..1017
270      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
272 GGATCCCCCG GTTCTCCCGG AAGGATTCGG GCGATGGCTG CAGGAGCGCG CCCCTCGGCC 60
274 CCATCAACCT GAGATGAGAA CAAC ATG AAG AAG AAG TCT CTG CTC CCC CTC 111
275      Met Lys Lys Lys Ser Leu Leu Pro Leu
276      -26 -25 -20
278 GGC CTG GCC ATC GGT CTC GCC TCT CTC GCT GCC AGC CCT CTG ATC CAG 159
279 Gly Leu Ala Ile Gly Leu Ala Ser Leu Ala Ala Ser Pro Leu Ile Gln
280      -15 -10 -5
282 GCC AGC ACC TAC ACC GAG ACC AAA TAC CCC ATC GTG CTG GCC CAC GGC 207
283 Ala Ser Thr Tyr Thr Gln Thr Lys Tyr Pro Ile Val Leu Ala His Gly
284      1 5 10 15
286 ATG CTC GGC TTC GAC AAC ATC CTC GGG GTC GAC TAC TGG TTC GGC ATT 255
287 Met Leu Gly Phe Asp Asn Ile Leu Gly Val Asp Tyr Trp Phe Gly Ile
288      20 25 30
290 CCC AGC GCC TTG CGC CGT GAC GGT GCC CAG GTC TAC GTC ACC GAA GTC 303
291 Pro Ser Ala Leu Arg Arg Asp Gly Ala Gln Val Tyr Val Thr Glu Val
292      35 40 45
294 AGC CAG TTG GAC ACC TCG GAA GTC CGC GGC GAG CAG TTG CTG CAA CAG 351
295 Ser Gln Leu Leu Asp Thr Ser Glu Val Arg Gly Glu Gln Leu Leu Gln Gln
296      50 55 60
298 GTG GAG GAA ATC GTC GCC CTC AGC GGC CAG CCC AAG GTC AAC CTG ATC 399
299 Val Glu Glu Ile Val Ala Leu Ser Gly Gln Pro Lys Val Asn Leu Ile
300      65 70 75
302 GGC CAC AGC CAC GGC GGG CCG ACC ATC CGC TAC GTC GCC GCC GTA CGT 447
303 Gly His Ser His Gly Gly Pro Thr Ile Arg Tyr Val Ala Ala Val Arg
304      80 85 90 95
306 CCC GAC CTG ATC GCT TCC GCC ACC AGC GTC GGC GCC CCG CAC AAG GGT 495
307 Pro Asp Leu Ile Ala Ser Ala Thr Ser Val Gly Ala Pro His Lys Gly
308      100 105 110
310 TCG GAC ACC GCC GAC TTC CTG CGC CAG ATC CCA CCG GGT TCG GCC GGC 543
311 Ser Asp Thr Ala Asp Phe Leu Arg Gln Ile Pro Pro Gly Ser Ala Gly
312      115 120 125
314 GAG GCA GTC CTC TCC GGG CTG GTC AAC AGC CTC GGC GCG CTG ATC AGC 591
315 Glu Ala Val Leu Ser Gly Leu Val Asn Ser Leu Gly Ala Leu Ile Ser
316      130 135 140
318 TTC CTT TCC AGC GGC GGC ACC GGT ACG CAG AAT TCA CTG GGC TCG CTG 639
319 Phe Leu Ser Ser Gly Gly Thr Gly Thr Gln Asn Ser Leu Gly Ser Leu
320      145 150 155
322 GAG TCG CTG AAC AGC GAG GGT GCC GCG CGC TTC AAC GCC AAG TAC CCG 687
323 Glu Ser Leu Asn Ser Glu Gly Ala Ala Arg Phe Asn Ala Lys Tyr Pro
324      160 165 170 175
327 CAG GGC ATC CCC ACC TCG GCC TGC GGC GAA GGC GCC TAC AAG GTC AAC 735
328 Gln Gly Ile Pro Thr Ser Ala Cys Gly Glu Gly Ala Tyr Lys Val Asn
329      180 185 190
331 GGC GTG AGC TAT TAC TCC TGG AGC GGT TCC TCG CCG CTG ACC AAC TTC 783
332 Gly Val Ser Tyr Tyr Ser Trp Ser Gly Ser Ser Pro Leu Thr Asn Phe
333      195 200 205

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## VERIFICATION SUMMARY

DATE: 03/07/2002

PATENT APPLICATION: US/09/463,494A

TIME: 11:06:18

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\03072002\I463494A.raw

L:11 M:220 C: Keyword misspelled or invalid format, [(iv) CORRESPONDENCE ADDRESS:]

L:24 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:25 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:1545 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:21

← delete the number  
"1" at the very  
end.